

SEQUENCE SUBMISSION

SEQ ID NO: 1 is mouse 499E9 nucleic acid sequence.

SEQ ID NO: 2 is mouse 499E9 amino acid sequence.

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(1) GENERAL INFORMATION:

(i) APPLICANT: Gorman, Daniel M.
Mattson, Jeanine D.

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(ii) TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
Reagents

(iii) NUMBER OF SEQUENCES: 2

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(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute
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(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1104

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE: 12-DEC-1997
(C) CLASSIFICATION:

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/032,846
(B) FILING DATE: 13-DEC-1996

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.
(B) REGISTRATION NUMBER: 34,090
(C) REFERENCE/DOCKET NUMBER: DX0686

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650)852-9196
(B) TELEFAX: (650)496-1200

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(2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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/62121-2968680

(ii) MOLECULE TYPE: cDNA

5 (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 125..1072

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GCCAGGACCT CTGTGAACCG GTCGGGGCGG GGGCCGCCTG GCCGGGAGTC TGCTCGGCGG      60
TGGGTGGCCG AGGAAGGGAG AGAACGATCG CGGAGCAGGG CGCCCCAACT CCGGGCGCCG      120
CGCC ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG TAC CTG CGC AGC TCG      169
  Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser
    1             5             10             15

GAG GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC GAG GGT CCG CTG CAC      217
Glu Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His
          20             25             30

CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA CCC GCC GCC TCC CGC      265
Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg
          35             40             45

TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG GGC CAG GTG GTC TGC      313
Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys
          50             55             60

AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG ATG GAT CCT AAC AGA      361
Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg
          65             70             75

ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA ATC CTG AGA CTC CAT      409
Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His
          80             85             90             95

GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG AGT GAA GAC ACA CTA      457
Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu
          100             105             110

CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT CAG GGG GCC GTG CAG      505
Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln
          115             120             125

AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC TTC TCA GGA GCT CCA      553
Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro
          130             135             140

GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC CAG CGA GGC AAG CCT      601
Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro
          145             150             155

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	GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT GCT GCC AGC ATC CCA	649
	Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro	
	160 165 170 175	
5	TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG TAC CAC GAT CGA GGC	697
	Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly	
	180 185 190	
10	TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC GGA AAA CTA AGG GTT	745
	Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val	
	195 200 205	
15	AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC ATT TGC TTT CGG CAT	793
	Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His	
	210 215 220	
20	CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT CTT CAG CTG ATG GTG	841
	His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val	
	225 230 235	
25	TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT AAC CTG ATG	889
	Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met	
	240 245 250 255	
30	AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT TCT GAA TTC CAC TTT	937
	Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe	
	260 265 270	
35	TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC CGA GCT GGT GAA GAA	985
	Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu	
	275 280 285	
40	ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG GAT CCG GAT CAA GAT	1033
	Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp	
	290 295 300	
45	GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC ATA GAC TGAGACTCAT	1082
	Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp	
	305 310 315	
50	TTCGTGGAAC ATTAGCATGG ATGTCCTAGA TGTTTGGAAC CTTCCTTAAAA AATGGATGAT	1142
	GTCTATACAT GTGTAAGACT ACTAAGAGAC ATGGCCACG GTGTATGAAA CTCACAGCCC	1202
55	TCTCTCTTGA GCCTGTACAG GTTGTGTATA TGTAAGTCC ATAGGTGATG TTAGATTTCAT	1262
	GGTGATTACA CAACGGTTTT ACAATTTTGT AATGATTTC TAAGAATTGA ACCAGATTGG	1322
	GAGAGGTATT CCGATGCTTA TGAAAACTT ACACGTGAGC TATGGAAGGG GGTCACAGTC	1382
	TCTGGGTCTA ACCCCTGGAC ATGTGCCACT GAGAACCTTG AAATTAAGAA GATGCCATGT	1442
	CATTGCAAAG AAATGATAGT GTGAAGGGTT AAGTTCTTTT GAATTGTTAC ATTGCGCTGG	1502
	GACCTGCAAA TAAGTTCTTT TTTTCTAATG AGGAGAGAAA AATATATGTA TTTTATATA	1562

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	ATGTCTAAAG	TTATATTTCA	GGTGTAATGT	TTTCTGTGCA	AAGTTTTGTA	AATTATATTT	1622
5	GTGCTATAGT	ATTTGATTCA	AAATATTTAA	AAATGTCTCA	CTGTTGACAT	ATTTAATGTT	1682
	TTAAATGTAC	AGATGTATTT	AACTGGTGCA	CTTTGTAATT	CCCCTGAAGG	TACTCGTAGC	1742
	TAAGGGGGCA	GAATACTGTT	TCTGGTGACC	ACATGTAGTT	TATTTCTTTA	TTCTTTTTTAA	1802
10	CTTAATAGAG	TCTTCAGACT	TGTCAAACT	ATGCAAGCAA	AATAAATAAA	TAAAAATAAA	1862
	ATGAATATCT	TGAATAATAA	GTAGGATGTT	GGTCACCAGG	TGCCTTTCAA	ATTTAGAAGC	1922
15	TAATTGACTT	TAGGAGCTGA	CATAGCCAAA	AAGGATACAT	AATAGGCTAC	TGAAAATCTG	1982
	TCAGGAGTAT	TTATGCAATT	ATTGAACAGG	TGTCTTTTTT	TACAAGAGCT	ACAAATTGTA	2042
	AATTTTGTTT	CTTTTTTTTC	CCATAGAAAA	TGTACTATAG	TTTATCAGCC	AAAAACAAT	2102
20	CCACTTTTTA	ATTTAGTGAA	AGTTATTTTA	TTATACTGTA	CAATAAAAAGC	ATTGTTTCTG	2162
	AATGGCATTT	TTTGGTACTT	AAAAATGGC				2191

25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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35      Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
        1             5             10             15
40      Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
              20             25             30
        Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Ala Ala Ser Arg Ser
              35             40             45
45      Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
        50             55             60
        Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
        65             70             75             80
50      Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
              85             90             95
        Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
        100             105             110

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